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 ********** STN Columbus **********
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FILE 'HOME' ENTERED AT 12:56:27 ON 25 MAR 2001

=> file medline

COST IN U.S. DOLLARS                SINCE FILE     TOTAL
                                    ENTRY   SESSION
FULL ESTIMATED COST                   0.15      0.15

FILE 'MEDLINE' ENTERED AT 12:56:33 ON 25 MAR 2001

 FILE LAST UPDATED: 22 MAR 2001 (20010322/UP). FILE
COVERS 1958 TO DATE.

 MEDLINE now contains new records from the former NLM
HEALTH STAR
 database. These records have an Entry Date and Update Date of
20010223.

 MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
 MeSH 2001 vocabulary. Enter HELP THESAURUS for details.

 The OLDMEDLINE file segment now contains data from 1958
through 1965.
 Enter HELP CONTENT for details.

 Left, right, and simultaneous left and right truncation are available in
the
 Basic Index. See HELP SFIELDS for details.

 THIS FILE CONTAINS CAS REGISTRY NUMBERS FOR EASY
AND ACCURATE
 SUBSTANCE IDENTIFICATION.

 MEDLINE has been updated with new records for the 2001
production year
 (20010322/UP). NLM is still in the process of preparing data.
Therefore,
 regular updates to the file are not in place. As soon as NLM makes
the
 regular updates available, we will process the update.

=> s methyltransferase and chimer?/ab,bi

      10153 METHYLTRANSFERASE
      25292 CHIMER?/BI
    5621341 AB/FA
      17441 CHIMER?/AB
            (CHIMER?/BI (L) AB/FA)
      25292 CHIMER?/BI
L1       57 METHYLTRANSFERASE AND CHIMER?/AB,BI

=> s l1 and cpg?/ab,bi

       4016 CPG?/BI
    5621341 AB/FA
       3696 CPG?/AB
            (CPG?/BI (L) AB/FA)
       4016 CPG?/BI
L2        1 L1 AND CPG?/AB,BI

=> d bib ab


L2  ANSWER 1 OF 1  MEDLINE
AN  96154196    MEDLINE
DN  96154196
TI  The methyl- ***CpG***  binding protein MeCP2 is essential
for embryonic
    development in the mouse.
AU  Tate P; Skarnes W; Bird A
CS  Institute of Cell and Molecular Biology, University of Edinburgh,
UK.
SO  NATURE GENETICS, (1996 Feb) 12 (2) 205-8.
    Journal code: BRO. ISSN: 1061-4036.
CY  United States
DT  Journal; Article; (JOURNAL ARTICLE)
LA  English
FS  Priority Journals
EM  199605
AB  Vertebrate genomes are heavily methylated at cytosines in the
sequence
     ***CpG***  . The biological role of this modification is probably
mediated
    by DNA binding proteins that are either attracted to or repelled by
    methyl- ***CpG***  . MeCP2 is an abundant chromosomal
protein that binds
    specifically to methylated DNA in vitro, and depends upon methyl-
     ***CpG***  for its chromosomal distribution in vivo. To assess
the
    functional significance of MeCP2, the X-linked gene was mutated
in male
    mouse embryonic stem (ES) cells using a promoterless
gene-targeting
    construct containing a lacZ reporter gene. Mutant ES cells lacking
MeCP2
    grew with the same vigour as the parental line and were capable of
    considerable differentiation. Chimaeric embryos derived from
several
    independent mutant lines, however, exhibited developmental
defects whose
    severity was positively correlated with the contribution of mutant
cells.
    The results demonstrate that MeCP2, like DNA
***methyltransferase*** ,
    is dispensable in stem cells, but essential for embryonic
development.


=> d kwic

L2  ANSWER 1 OF 1  MEDLINE
TI  The methyl- ***CpG***  binding protein MeCP2 is essential
for embryonic
    development in the mouse.
AB  Vertebrate genomes are heavily methylated at cytosines in the
sequence
     ***CpG***  . The biological role of this modification is probably
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    methyl- ***CpG***  . MeCP2 is an abundant chromosomal
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    specifically to methylated DNA in vitro, and depends upon methyl-
     ***CpG***  for its chromosomal distribution in vivo. To assess
the
    functional significance of MeCP2, the X-linked gene was mutated
in male.
    . . developmental defects whose severity was positively correlated
with
    the contribution of mutant cells. The results demonstrate that
MeCP2, like
    DNA  ***methyltransferase***  , is dispensable in stem cells, but
    essential for embryonic development.
CT  Check Tags: Animal; Male; Support, Non-U.S. Gov't
    beta-Galactosidase: BI, biosynthesis
    beta-Galactosidase: GE, genetics
     *** Chimera***
    DNA-Binding Proteins: GE, genetics
    *DNA-Binding Proteins: PH, physiology
    *Fetal Development: PH, physiology
    Gene Targeting
    Linkage (Genetics)
    Mice
    Recombinant Fusion. . .


=> s l1 and lex?/ab,bi

       4774 LEX?/BI
    5621341 AB/FA
       4065 LEX?/AB
            (LEX?/BI (L) AB/FA)
       4774 LEX?/BI
L3        0 L1 AND LEX?/AB,BI

=> s zinc finger and methyltransferase#/ab,bi

      45825 ZINC
      24408 FINGER
       3942 ZINC FINGER
            (ZINC(W)FINGER)
      12084 METHYLTRANSFERASE#/BI
    5621341 AB/FA
       5992 METHYLTRANSFERASE#/AB
            (METHYLTRANSFERASE#/BI (L) AB/FA)
      12084 METHYLTRANSFERASE#/BI
L4        9 ZINC FINGER AND
```

METHYLTRANSFERASE#/AB,BI

=> s l4 and (fusion or chimer?)/ab,bi

82973 FUSION/BI
5621341 AB/FA
49946 FUSION/AB
(FUSION/BI (L) AB/FA)
82973 FUSION/BI
25292 CHIMER?/BI
5621341 AB/FA
17441 CHIMER?/AB
(CHIMER?/BI (L) AB/FA)
25292 CHIMER?/BI
L5 1 L4 AND (FUSION OR CHIMER?)/AB,BI

=> d bib ab

L5 ANSWER 1 OF 1 MEDLINE
AN 2001031129 MEDLINE
DN 20490738
TI PRMT3 is a distinct member of the protein arginine N-***methyltransferase*** family. Conferral of substrate specificity by a ***zinc*** - ***finger*** domain.
AU Frankel A; Clarke S
CS Molecular Biology Institute and the Department of Chemistry & Biochemistry, University of California at Los Angeles, California 90095, USA.
NC GM26020 (NIGMS)
T32 GM07185 (NIGMS)
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Oct 20) 275 (42) 32974-82.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200011
AB S-Adenosyl-l-methionine-dependent protein arginine N-***methyltransferases*** (PRMTs) catalyze the methylation of arginine residues within a variety of proteins. At least four distinct mammalian family members have now been described, including PRMT1, PRMT3, CARM1/PRMT4, and JBP1/PRMT5. To more fully define the physiological role of PRMT3, we characterized its unique putative ***zinc*** - ***finger*** domain and how it can affect its enzymatic activity. Here we show that PRMT3 does contain a single ***zinc*** - ***finger*** domain in its amino terminus. Although the zinc-liganded form of this domain is not required for methylation of an artificial substrate such as the glutathione S-transferase-fibrillarin amino-terminal ***fusion*** protein (GST-GAR), it is required for the enzyme to recognize RNA-associated substrates in RAT1 cell extracts. The recombinant form of PRMT3 is inhibited by high concentrations of ZnCl(2) as well as N-ethylmaleimide, reagents that can modify cysteine sulfhydryl groups. We found that we could distinguish PRMT family members by their sensitivity to these reagents; JBP1/PRMT5 and Hsl7 ***methyltransferases*** were inhibited in a similar manner as PRMT3, whereas Rmt1, PRMT1, and CARM1/PRMT4 were not affected. We were also able to define differences in these enzymes by their sensitivity to inhibition by Tris and free arginine. Finally, we found that the treatment of RAT1 cell extracts with N-ethylmaleimide leads to a loss of the major PRMT1-associated activity that was immune to inhibition under the same conditions as a GST ***fusion*** protein. These results suggest that native forms of PRMTs can have different properties than their GST-catalytic chain ***fusion*** protein counterparts, which may lack associated noncatalytic subunits.

=> file medline embase biosis inpadoc caplus

COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION
FULL ESTIMATED COST 2.55 2.70

FILE 'MEDLINE' ENTERED AT 13:00:32 ON 25 MAR 2001

FILE 'EMBASE' ENTERED AT 13:00:32 ON 25 MAR 2001
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FILE 'INPADOC' ENTERED AT 13:00:32 ON 25 MAR 2001
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=> e bestor t/ab,bi

EXPAND COMMAND IS NOT AVAILABLE FOR THIS FIELD:
AB
EXPAND COMMAND IS NOT AVAILABLE FOR THIS FIELD:
AB
'AB' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'BIOSIS'
E1 5 BESTOR/BI
E2 0 --> BESTOR T/AB
E3 0 --> BESTOR T/BI
E4 2 BESTORED/AB
E5 1 BESTORED/BI
E6 1 BESTORPENSIS/BI
E7 4 BESTORTEN/BI
E8 2 BESTOS/AB
E9 2 BESTOS/BI
E10 1 BESTOSSHOBEL/BI
E11 1 BESTOUS/BI
The indicated field code is not available for EXPAND in this file. To see a list of valid EXPAND field codes, enter HELP SFIELDS at an arrow prompt (=>).

=> e bestor t/au

E1 1 BESTON PERCIVAL G/AU
E2 2 BESTOR D K/AU
E3 26 --> BESTOR T/AU
E4 104 BESTOR T H/AU
E5 2 BESTOR TIM/AU
E6 10 BESTOR TIMOTHY/AU
E7 81 BESTOR TIMOTHY H/AU
E8 1 BESTOR TIMOTHY HENRY/AU
E9 1 BESTOR W/AU
E10 1 BESTOR W E/AU
E11 3 BESTOSO JOHN T/AU
E12 1 BESTOSO W J/AU

=> s e3-e8

L6 224 ("BESTOR T"/AU OR "BESTOR T H"/AU OR "BESTOR TIM"/AU OR "BESTOR TIMOTHY"/AU OR "BESTOR TIMOTHY H"/AU OR "BESTOR TIMOTHY HENRY"/AU)

=> d his

(FILE 'HOME' ENTERED AT 12:56:27 ON 25 MAR 2001)

FILE 'MEDLINE' ENTERED AT 12:56:33 ON 25 MAR 2001
L1 57 S METHYLTRANSFERASE AND CHIMER?/AB,BI
L2 1 S L1 AND CPG?/AB,BI
L3 0 S L1 AND LEX?/AB,BI
L4 9 S ZINC FINGER AND METHYLTRANSFERASE#/AB,BI
L5 1 S L4 AND (FUSION OR CHIMER?)/AB,BI

FILE 'MEDLINE, EMBASE, BIOSIS, INPADOC, CAPLUS'

ENTERED AT 13:00:32 ON 25
MAR 2001
E BESTOR T/AB,BI
E BESTOR T/AU
L6 224 S E3-E8

=> s l1 and l6

'AB' IS NOT A VALID FIELD CODE
L7 5 L1 AND L6

=> dup rem l7

PROCESSING COMPLETED FOR L7
L8 4 DUP REM L7 (1 DUPLICATE REMOVED)

=> d 1- bib ab

YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):y

L8 ANSWER 1 OF 4 INPADOC COPYRIGHT 2001 EPO
DUPLICATE 1

LEVEL 1
AN 42035735 INPADOC UP 20010206 UW 200105
TI ***CHIMERIC*** DNA-BINDING/DNA ***METHYLTRANSFERASE*** NUCLEIC ACID AND POLYPEPTIDE AND USES THEREOF
IN BESTOR, TIMOTHY, H.
INS ***BESTOR TIMOTHY H***
INA US
PA THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF; BESTOR, TIMOTHY, H.
PAS UNIV COLUMBIA; BESTOR TIMOTHY H
PAA US; US
TL English; French
LA English
DT Patent
PIT WOA1 PUBL.OF THE INT.APPL. WITH INT.SEARCH REPORT
PI WO 9711972 A1 19970403
DS RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: AU CA JP MX US US
AI WO 1996-US15576 A 19960927
PRAI US 1995-4445 A2 19950928
US 1996-594866 A2 19960131
OSDW 97-212856
AB The present invention provides a ***chimeric*** protein which comprises a mutated DNA methyltransferase portion and a DNA binding protein portion that binds sufficiently close to a promoter sequence of a target gene which promoter sequence contains a methylation site, to specifically methylate the site and inhibit activity of the promoter and thus inhibit expression of the target gene. This invention also provides for a method for inhibiting the expression of a target gene which includes contacting a promoter of the target gene with the ***chimeric*** protein, so as to specifically methylate the promoter sequence of the target gene thus inhibiting expression of the target gene.

L8 ANSWER 2 OF 4 INPADOC COPYRIGHT 2001 EPO

LEVEL 1
AN 12181505 INPADOC
TI ***CHIMERIC*** DNA-BINDING/DNA ***METHYLTRANSFERASE*** NUCLEIC ACID AND POLYPEPTIDE AND USES THEREOF
IN TIMOTHY H. BESTOR
INS ***BESTOR TIMOTHY H***
PA THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
PAS UNIV COLUMBIA
DT Patent
PIT AUA1 COMP. SPEC. OPEN TO PUB. INSP.
PI AU 9673781 A1 19970417
AI AU 1996-73781 A 19960927
PRAI US 1995-4445 P 19950928
US 1996-594866 A 19960131
WO 1996-US15576 W 19960927

L8 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2001 ACS
AN 1997:791788 CAPLUS
DN 128:111239
TI Cytosine methylation targeted to pre-determined sequences
AU Xu, Guo-Liang; ***Bestor, Timothy H.***
CS Department of Genetics and Development, College of Physicians and Surgeons of Columbia University, New York, NY, 10032, USA
SO Nat. Genet. (1997), 17(4), 376-378
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal
LA English
AB Predetd. sequence specificities have now been conferred upon a DNA ***methyltransferase*** by fusion to zinc-finger proteins. The sequence specificity of zinc-finger proteins can be modified to direct cytosine methylation to the promoters of target genes. Targeted methylation is proposed as a new method for selective gene inactivation that stimulates an existing biol. response.

L8 ANSWER 4 OF 4 MEDLINE

AN 92298390 MEDLINE
DN 92298390
TI Targeted mutation of the DNA ***methyltransferase*** gene results in embryonic lethality.
AU Li E; ***Bestor T H*** ; Jaenisch R
CS Whitehead Institute for Biomedical Research, Cambridge, Massachusetts 02142..
NC GM43565 (NIGMS)
R35 CA 44339-05 (NCI)
SO CELL, (1992 Jun 12) 69 (6) 915-26.
Journal code: CQ4. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199209
AB Gene targeting in embryonic stem (ES) cells has been used to mutate the murine DNA ***methyltransferase*** gene. ES cell lines homozygous for the mutation were generated by consecutive targeting of both wild-type alleles; the mutant cells were viable and showed no obvious abnormalities with respect to growth rate or morphology, and had only trace levels of DNA ***methyltransferase*** activity. A quantitative end-labeling assay showed that the level of m5C in the DNA of homozygous mutant cells was about one-third that of wild-type cells, and Southern blot analysis after cleavage of the DNA with a methylation-sensitive restriction endonuclease revealed substantial demethylation of endogenous retroviral DNA. The mutation was introduced into the germline of mice and found to cause a recessive lethal phenotype. Homozygous embryos were stunted, delayed in development, and did not survive past mid-gestation. The DNA of homozygous embryos showed a reduction of the level of m5C similar to that of homozygous ES cells. These results indicate that while a 3-fold reduction in levels of genomic m5C has no detectable effect on the viability or proliferation of ES cells in culture, a similar reduction of DNA methylation in embryos causes abnormal development and embryonic lethality.

=> s methyltransferase# and (fusion or chimer?)/ab,bi

'AB' IS NOT A VALID FIELD CODE

L9 777 METHYLTRANSFERASE# AND (FUSION OR CHIMER?)/AB,BI

=> s l9 and cpg/ab,bi

'AB' IS NOT A VALID FIELD CODE
L10 16 L9 AND CPG/AB,BI

=> dup rem l10

PROCESSING COMPLETED FOR L10
L11 9 DUP REM L10 (7 DUPLICATES REMOVED)

=> d 1- bib ab

YOU HAVE REQUESTED DATA FROM 9 ANSWERS - CONTINUE? Y/(N):y

L11 ANSWER 1 OF 9 MEDLINE
AN 2000497370 MEDLINE
DN 20440199
TI Transcriptional repression by Drosophila methyl- ***CpG*** -binding
proteins.
AU Roder K; Hung M S; Lee T L; Lin T Y; Xiao H; Isobe K I; Juang J L; Shen C
J
CS Institute of Molecular Biology, Academia Sinica, Nankang, Taipei, Taiwan,
Republic of China.
SO MOLECULAR AND CELLULAR BIOLOGY, (2000 Oct) 20 (19) 7401-9.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200012
EW 20001204
AB C methylation at genomic ***CpG*** dinucleotides has been implicated
in the regulation of a number of genetic activities during vertebrate cell
differentiation and embryo development. The methylated ***CpG*** could
induce chromatin condensation through the recruitment of histone
deacetylase (HDAC)-containing complexes by methyl- ***CpG*** -binding
proteins. These proteins consist of the methylated-DNA binding domain
(MBD). Unexpectedly, however, several studies have identified
MBD-containing proteins encoded by genes of Drosophila melanogaster, an
invertebrate species supposed to be void of detectable m(5) ***CpG*** .
We now report the genomic structure of a Drosophila gene, dMBD2/3, that
codes for two MBD-containing, alternatively spliced, and developmentally
regulated isoforms of proteins, dMBD2/3 and dMBD2/3Delta. Interestingly,
in vitro binding experiments showed that as was the case for vertebrate
MBD proteins, dMBD2/3Delta could preferentially recognize m(5) ***CpG***
-containing DNA through its MBD. Furthermore, dMBD2/3Delta as well as one
of its orthologs in mouse, MBD2b, could function in human cells as a
transcriptional corepressor or repressor. The activities of HDACs appeared
to be dispensable for transcriptional repression by dMBD2/3Delta. Finally,
dMBD2/3Delta also could repress transcription effectively in transfected
Drosophila cells. The surprisingly similar structures and characteristics
of the MBD proteins as well as DNA cytosine (C-5) ***methyltransferase*** -related proteins in Drosophila and vertebrates
suggest interesting scenarios for their roles in eukaryotic cellular
functions.

L11 ANSWER 2 OF 9 MEDLINE
AN 2000391949 MEDLINE
DN 20347723
TI DNMT1 forms a complex with Rb, E2F1 and HDAC1 and represses transcription
from E2F-responsive promoters.
AU Robertson K D; Ait-Si-Ali S; Yokochi T; Wade P A; Jones P L; Wolffe A P
CS Laboratory of Molecular Embryology, NICHD, NIH, Bethesda, Maryland, USA.
SO NATURE GENETICS, (2000 Jul) 25 (3) 338-42.
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200010
EW 20001003
AB Methylation of ***CpG*** islands is associated with transcriptional
silencing and the formation of nuclease-resistant chromatin structures
enriched in hypoacetylated histones. Methyl- ***CpG*** -binding
proteins, such as MeCP2, provide a link between methylated DNA and
hypoacetylated histones by recruiting histone deacetylase, but the
mechanisms establishing the methylation patterns themselves are unknown.
Whether DNA methylation is always causal for the assembly of repressive
chromatin or whether features of transcriptionally silent chromatin might
target ***methyltransferase*** remains unresolved. Mammalian DNA
methyltransferases show little sequence specificity in vitro, yet
methylation can be targeted in vivo within chromosomes to repetitive
elements, centromeres and imprinted loci. This targeting is frequently
disrupted in tumour cells, resulting in the improper silencing of
tumour-suppressor genes associated with ***CpG*** islands. Here we
show that the predominant mammalian DNA ***methyltransferase*** ,
DNMT1, co-purifies with the retinoblastoma (Rb) tumour suppressor gene
product, E2F1, and HDAC1 and that DNMT1 cooperates with Rb to repress
transcription from promoters containing E2F-binding sites. These results
establish a link between DNA methylation, histone deacetylase and
sequence-specific DNA binding activity, as well as a growth-regulatory
pathway that is disrupted in nearly all cancer cells.

L11 ANSWER 3 OF 9 MEDLINE
AN 2000082816 MEDLINE
DN 20082816
TI DNA ***methyltransferase*** Dnmt1 associates with histone deacetylase
activity.
AU Fuks F; Burgers W A; Brehm A; Hughes-Davies L; Kouzarides T
CS Wellcome/CRC Institute, Department of Pathology, Cambridge University,
Cambridge, UK.
SO NATURE GENETICS, (2000 Jan) 24 (1) 88-91.
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200004
EW 20000402
AB The DNA ***methyltransferase*** Dnmt1 is responsible for cytosine
methylation in mammals and has a role in gene silencing. DNA methylation
represses genes partly by recruitment of the methyl- ***CpG*** -binding
protein MeCP2, which in turn recruits a histone deacetylase activity. Here
we show that Dnmt1 is itself associated with histone deacetylase activity
in vivo. Consistent with this association, we find that one of the

known
histone deacetylases, HDAC1, has the ability to bind Dnmt1 and can purify
methyltransferase activity from nuclear extracts. We have
identified a transcriptional repression domain in Dnmt1 that functions, at
least partly, by recruiting histone deacetylase activity and shows
homology to the repressor domain of the trithorax-related protein HRX
(also known as MLL and ALL-1). Our data show a more direct connection
between DNA methylation and histone deacetylation than was previously
considered. We suggest that the process of DNA methylation, mediated by
Dnmt1, may depend on or generate an altered chromatin state via histone
deacetylase activity.

L11 ANSWER 4 OF 9 MEDLINE DUPLICATE 1
AN 2000056258 MEDLINE
DN 20056258
TI The DNMT3B DNA ***methyltransferase*** gene is mutated in the ICF
immunodeficiency syndrome.
AU Hansen R S; Wijmenga C; Luo P; Stanek A M; Canfield T K; Weemaes C M;
Gartler S M
CS Department of Medicine, University of Washington, Seattle, WA 98195, USA..
supreme@u.washington.edu
NC HD16659 (NICHD)
GM52463 (NIGMS)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
AMERICA, (1999 Dec 7) 96 (25) 14412-7.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 200003
EW 20000302
AB DNA methylation is an important regulator of genetic information in
species ranging from bacteria to humans. DNA methylation appears to be
critical for mammalian development because mice nullizygous for a targeted
disruption of the DNMT1 DNA ***methyltransferase*** die at an early
embryonic stage. No DNA ***methyltransferase*** mutations have been
reported in humans until now. We describe here the first example of
naturally occurring mutations in a mammalian DNA
methyltransferase
gene. These mutations occur in patients with a rare autosomal recessive
disorder, which is termed the ICF syndrome, for immunodeficiency,
centromeric instability, and facial anomalies. Centromeric instability of
chromosomes 1, 9, and 16 is associated with abnormal hypomethylation of
CpG sites in their pericentromeric satellite regions. We are able
to complement this hypomethylation defect by somatic cell ***fusion***
to Chinese hamster ovary cells, suggesting that the ICF gene is conserved
in the hamster and promotes de novo methylation. ICF has been localized to
a 9-centimorgan region of chromosome 20 by homozygosity mapping. By
searching for homologies to known DNA ***methyltransferases*** , we
identified a genomic sequence in the ICF region that contains the
homologue of the mouse Dnmt3b ***methyltransferase*** gene. Using the
human sequence to screen ICF kindreds, we discovered mutations in four
patients from three families. Mutations include two missense substitutions
and a 3-aa insertion resulting from the creation of a novel 3' splice
acceptor. None of the mutations were found in over 200 normal chromosomes.
We conclude that mutations in the DNMT3B are responsible for the ICF
syndrome.

L11 ANSWER 5 OF 9 MEDLINE
AN 1999449787 MEDLINE
DN 99449787
TI Drosophila proteins related to vertebrate DNA (5-cytosine)
methyltransferases .
AU Hung M S; Karthikeyan N; Huang B; Koo H C; Kiger J; Shen C J
CS Institute of Molecular Biology, Academia Sinica, Nankang, Taipei, Taiwan
115.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
AMERICA, (1999 Oct 12) 96 (21) 11940-5.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
OS GENBANK-AF185647
EM 200001
EW 20000104
AB DNA methylation at ***CpG*** residues is closely associated with a
number of biological processes during vertebrate development. Unlike the
vertebrates, however, several invertebrate species, including the
Drosophila, do not have apparent DNA methylation in their genomes. Nor
have there been reports on a DNA (5-cytosine) ***methyltransferase***
(***CpG*** MTase) found in these invertebrates. We now present
evidence for two ***CpG*** MTase-like proteins expressed in Drosophila
cells. One of these, DmMTR1, is a protein containing peptide epitopes
immunologically related to the conserved motifs I and IV in the catalytic
domain of the mammalian dnmt1. DmMTR1 has an apparent molecular mass of
220 kDa and, similar to mammalian dnmt1, it also interacts in vivo with
the proliferating cell nuclear antigen. During interphase of the syncytial
Drosophila embryos, the DmMTR1 molecules are located outside the nuclei,
as is dnmt1 in the mouse blastocyst. However, DmMTR1 appears to be rapidly
transported into, and then out of the nuclei again, as the embryos undergo
mitotic waves. Immunofluorescent data indicate that DmMTR1 molecules
"paint" the whole set of condensed Drosophila chromosomes throughout the
mitotic phase, suggesting they may play an essential function in the
cell-cycle regulated condensation of the Drosophila chromosomes. Through
search in the genomic database, we also have identified a Drosophila
polypeptide, DmMT2, that exhibits high sequence homology to the mammalian
dnmt2 and the yeast ***CpG*** MTase homolog pmt1. The expression of
DmMT2 appears to be developmentally regulated. We discuss the evolutionary
and functional implications of the discovery of these two Drosophila
proteins related to mammalian ***CpG*** MTases.

L11 ANSWER 6 OF 9 MEDLINE DUPLICATE 2
AN 2000047908 MEDLINE
DN 20047908
TI Isolation of the novel cDNA of a gene of which expression is induced by a
demethylating stimulus.
AU Miyagawa J; Muguruma M; Aoto H; Suetake I; Nakamura M; Tajima S
CS Institute for Protein Research, Osaka University, 3-2, Yamadaoka, Suita,

Osaka, Japan.
SO GENE, (1999 Nov 29) 240 (2) 289-95.
Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AB007141
EM 200003
EW 20000302
AB We have isolated a novel cDNA clone, named AZ2, from a cDNA library of
mRNA prepared from C3H10T1/2 cells that had been transiently exposed to
5-azacytidine, a potent inhibitor of DNA ***methyltransferase*** . The
elucidated nucleotide sequence revealed that the 5' region of the cDNA was
rich in the ***CpG*** sequence. The AZ2 cDNA contained a
1215-nucleotide open reading frame, and the expected amino acid sequence
had a molecular mass of 46090. The amount of the transcript increased on
5-azacytidine treatment of C3H10T1/2 cells, and the transcript was
significantly expressed in mouse testis, brain, lung, kidney, heart and
ovary. Specific antibodies raised against a ***fusion*** protein
including glutathione S-transferase revealed a band of an approximately
48kDa translation product for testis, brain, lung, and cultured cells that
ectopically expressed the AZ2 protein. The AZ2 protein was mainly
localized in the cytoplasm. The amino-terminal part of the AZ2 protein was
homologous to the previously reported TANK (Cheng and Baltimore, 1996.
Genes Dev. 10, 963-973) and I-TRAF (Rothe, 1996. Proc. Natl. Acad. Sci.
USA 93, 8241-8246), which participate in the signal transduction cascade
from the tumor necrosis factor-receptor to the transcription factor,
NFkappaB. Overexpression of AZ2 inhibited TNF alpha mediated NFkappaB
activation. AZ2 could be a component of a regulator of the NFkappaB
activation cascade.

L11 ANSWER 7 OF 9 MEDLINE
AN 1998378561 MEDLINE
DN 98378561
TI Methyl- ***CpG*** -binding protein MeCP2 represses Sp1-activated
transcription of the human leukosialin gene when the promoter is methylated.
AU Kudo S
CS Hokkaido Institute of Public Health, Kita-19, Nishi-12, Kita-ku, Sapporo
060-0819, Japan.. kudos@pref.iph.hokkaido.jp
SO MOLECULAR AND CELLULAR BIOLOGY, (1998 Sep) 18 (9) 5492-9.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L37298
EM 199811
AB Human leukosialin (CD43) is expressed in a cell lineage-specific as well
as a differentiation stage-specific fashion. The leukosialin promoter,
made up of an Sp1 binding site and a sequence similar to that of an
initiator, possesses high transcriptional potential. Previous data have
demonstrated that the leukosialin gene is down-regulated in nonproducing
cells by DNA methylation. In this paper the repressive mechanism of DNA
methylation in expression systems is reported. In vitro DNA methylation
with SssI (***CpG***) methylase of leukosialin-chloramphenicol
acetyltransferase (CAT) constructs drastically reduced transcriptional
activities in stable transfection systems with the human HeLa and Jurkat
cell lines. On the other hand, the transcriptional repression by in vitro
methylation was less pronounced in Drosophila melanogaster cells, which
lack genomic methylation. In these cells, Sp1 could transactivate equally
well both the unmethylated and methylated leukosialin promoter. In order
to test whether one of the methyl- ***CpG*** -binding proteins, MeCP2,
is responsible for transcriptional repression of the leukosialin gene, I
isolated the human MeCP2 cDNA (encoding 486 amino acid residues) and
expressed it in Drosophila cells. I found that MeCP2 substantially
inhibited Sp1-activated transcription when the leukosialin promoter was
methylated. The level of repression was directly proportional to the
amount of MeCP2 expression vector transfected. Analysis of C-terminal
deletion mutants of MeCP2 showed that repressive activity of Sp1
transactivation is localized to the N-terminal region consisting of amino
acid residues 1 to 193, which encompass the methyl-binding domain. These
results suggest that interference with Sp1 transactivation by MeCP2 is an
important factor in the down-regulation of leukosialin gene expression by
DNA methylation.

L11 ANSWER 8 OF 9 MEDLINE
AN 1998061079 MEDLINE
DN 98061079
TI Cytosine methylation targetted to pre-determined sequences [letter].
AU Xu G L; Bestor T H
NC GM00616 (NIGMS)
AI40021 (NIAID)
SO NATURE GENETICS, (1997 Dec) 17 (4) 376-8.
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Letter
LA English
FS Priority Journals
EM 199803
EW 19980301

L11 ANSWER 9 OF 9 MEDLINE DUPLICATE 3
AN 96154196 MEDLINE
DN 96154196
TI The methyl- ***CpG*** binding protein MeCP2 is essential for embryonic
development in the mouse.
AU Tate P; Skarnes W; Bird A
CS Institute of Cell and Molecular Biology, University of Edinburgh, UK.
SO NATURE GENETICS, (1996 Feb) 12 (2) 205-8.
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199605
AB Vertebrate genomes are heavily methylated at cytosines in the sequence
CpG . The biological role of this modification is probably mediated
by DNA binding proteins that are either attracted to or repelled by
methyl- ***CpG*** . MeCP2 is an abundant chromosomal protein that binds
specifically to methylated DNA in vitro, and depends upon methyl-
CpG for its chromosomal distribution in vivo. To assess the
functional significance of MeCP2, the X-linked gene was mutated in male
mouse embryonic stem (ES) cells using a promoterless gene-targeting
construct containing a lacZ reporter gene. Mutant ES cells lacking MeCP2
grew with the same vigour as the parental line and were capable of
considerable differentiation. Chimaeric embryos derived from several
independent mutant lines, however, exhibited developmental

defects whose
severity was positively correlated with the contribution of mutant cells.
The results demonstrate that MeCP2, like DNA ***methyltransferase*** ,
is dispensable in stem cells, but essential for embryonic development.

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(FILE 'HOME' ENTERED AT 12:56:27 ON 25 MAR 2001)

FILE 'MEDLINE' ENTERED AT 12:56:33 ON 25 MAR 2001
L1 57 S METHYLTRANSFERASE AND CHIMER?/AB,BI
L2 1 S L1 AND CPG?/AB,BI
L3 0 S L1 AND LEX?/AB,BI
L4 9 S ZINC FINGER AND METHYLTRANSFERASE#/AB,BI
L5 1 S L4 AND (FUSION OR CHIMER?)/AB,BI

FILE 'MEDLINE, EMBASE, BIOSIS, INPADOC, CAPLUS' ENTERED AT 13:00:32 ON 25
MAR 2001
E BESTOR T/AB,BI
E BESTOR T/AU
L6 224 S E3-E8
L7 5 S L1 AND L6
L8 4 DUP REM L7 (1 DUPLICATE REMOVED)
L9 777 S METHYLTRANSFERASE# AND (FUSION OR CHIMER?)/AB,BI
L10 16 S L9 AND CPG/AB,BI
L11 9 DUP REM L10 (7 DUPLICATES REMOVED)

=> s l9 and l6

L12 20 L9 AND L6

=> dup rem l12

PROCESSING COMPLETED FOR L12
L13 9 DUP REM L12 (11 DUPLICATES REMOVED)

=> d 1- bib ab

YOU HAVE REQUESTED DATA FROM 9 ANSWERS - CONTINUE? Y/(N):y

L13 ANSWER 1 OF 9 MEDLINE
AN 1998061079 MEDLINE
DN 98061079
TI Cytosine methylation targetted to pre-determined sequences [letter].
AU Xu G L; ***Bestor T H***
NC GM00616 (NIGMS)
AI40021 (NIAID)
SO NATURE GENETICS, (1997 Dec) 17 (4) 376-8.
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Letter
LA English
FS Priority Journals
EM 199803
EW 19980301

L13 ANSWER 2 OF 9 INPADOC COPYRIGHT 2001 EPO DUPLICATE 1

LEVEL 1
AN 42035735 INPADOC UP 20010206 UW 200105
TI ***CHIMERIC*** DNA-BINDING/DNA ***METHYLTRANSFERASE*** NUCLEIC
ACID AND POLYPEPTIDE AND USES THEREOF
IN BESTOR, TIMOTHY, H.
INS ***BESTOR TIMOTHY H***
INA US
PA THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF; BESTOR, TIMOTHY, H.
PAS UNIV COLUMBIA; BESTOR TIMOTHY H
PAA US; US
TL English; French
LA English
DT Patent
PIT WOA1 PUBL.OF THE INT.APPL. WITH INT.SEARCH REPORT
PI WO 9711972 A1 19970403
DS RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: AU CA JP MX US US
AI WO 1996-US15576 A 19960927
PRAI US 1995-4445 A2 19950928
US 1996-594866 A2 19960131
OSDW 97-212856
AB The present invention provides a ***chimeric*** protein which
comprises a mutated DNA methyltransferase portion and a DNA binding
protein portion that binds sufficiently close to a promoter sequence of a
target gene which promoter sequence contains a methylation site, to
specifically methylate the site and inhibit activity of the promoter and
thus inhibit expression of the target gene. This invention also provides
for a method for inhibiting the expression of a target gene which
includes contacting a promoter of the target gene with the
chimeric protein, so as to specifically methylate the promoter
sequence of the target gene thus inhibiting expression of the target gene.

L13 ANSWER 3 OF 9 INPADOC COPYRIGHT 2001 EPO

LEVEL 1
AN 12181505 INPADOC
TI ***CHIMERIC*** DNA-BINDING/DNA ***METHYLTRANSFERASE*** NUCLEIC
ACID AND POLYPEPTIDE AND USES THEREOF
IN TIMOTHY H. BESTOR
INS ***BESTOR TIMOTHY H***
PA THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
PAS UNIV COLUMBIA
DT Patent
PIT AUA1 COMP. SPEC. OPEN TO PUB. INSP.
PI AU 9673781 A1 19970417
AI AU 1996-73781 A 19960927
PRAI US 1995-4445 P 19950928
US 1996-594866 A 19960131
WO 1996-US15576 W 19960927

L13 ANSWER 4 OF 9 CAPLUS COPYRIGHT 2001 ACS
AN 1997:791788 CAPLUS
DN 128:111239
TI Cytosine methylation targeted to pre-determined sequences
AU Xu, Guo-Liang; ***Bestor, Timothy H.***
CS Department of Genetics and Development, College of Physicians and Surgeons
of Columbia University, New York, NY, 10032, USA
SO Nat. Genet. (1997), 17(4), 376-378
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal
LA English
AB Predetd. sequence specificities have now been conferred upon a DNA
methyltransferase by ***fusion*** to zinc-finger proteins.
The sequence specificity of zinc-finger proteins can be modified to direct
cytosine methylation to the promoters of target genes. Targeted
methylation is proposed as a new method for selective gene inactivation
that stimulates an existing biol. response.

L13 ANSWER 5 OF 9 MEDLINE DUPLICATE 2
AN 92331613 MEDLINE
DN 92331613
TI Activation of mammalian DNA ***methyltransferase*** by cleavage of a
Zn binding regulatory domain.
AU ***Bestor T H***
CS Department of Anatomy and Cellular Biology, Harvard Medical School,
Boston, MA 02115.
NC GM43565 (NIGMS)
SO EMBO JOURNAL, (1992 Jul) 11 (7) 2611-7.
Journal code: EMB. ISSN: 0261-4189.

CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199210
AB Mammalian DNA (cytosine-5) ***methyltransferase*** contains a
C-terminal domain that is closely related to bacterial cytosine-5
restriction ***methyltransferase*** . This ***methyltransferase***
domain is linked to a large N-terminal domain. It is shown here that the
N-terminal domain contains a Zn binding site and that the N- and
C-terminal domains can be separated by cleavage with trypsin or
Staphylococcus aureus protease V8; the protease V8 cleavage site was
determined by Edman degradation to lie 10 residues C-terminal of the run
of alternating lysyl and glycyl residues which joins the two domains and
six residues N-terminal of the first sequence motif conserved between the
mammalian and bacterial cytosine ***methyltransferases*** . While the
intact enzyme had little activity on unmethylated DNA substrates, cleavage
between the domains caused a large stimulation of the initial velocity of
methylation of unmethylated DNA without substantial change in the rate of
methylation of hemimethylated DNA. These findings indicate that the
N-terminal domain of DNA ***methyltransferase*** ensures the clonal
propagation of methylation patterns through inhibition of the de novo
activity of the C-terminal domain. Mammalian DNA ***methyltransferase***
is likely to have arisen via ***fusion*** of a prokaryotic-like
restriction ***methyltransferase*** and an unrelated DNA binding
protein. Stimulation of the de novo activity of DNA
methyltransferase by proteolytic cleavage in vivo may contribute
to the process of ectopic methylation observed in the DNA of aging
animals, tumors and in lines of cultured cells.

L13 ANSWER 6 OF 9 MEDLINE
AN 92298390 MEDLINE
DN 92298390
TI Targeted mutation of the DNA ***methyltransferase*** gene results in
embryonic lethality.
AU Li E; ***Bestor T H*** ; Jaenisch R
CS Whitehead Institute for Biomedical Research, Cambridge, Massachusetts
02142..
NC GM43565 (NIGMS)
R35 CA 44339-05 (NCI)
SO CELL, (1992 Jun 12) 69 (6) 915-26.
Journal code: CQ4. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199209
AB Gene targeting in embryonic stem (ES) cells has been used to mutate the
murine DNA ***methyltransferase*** gene. ES cell lines homozygous for
the mutation were generated by consecutive targeting of both wild-type
alleles; the mutant cells were viable and showed no obvious abnormalities
with respect to growth rate or morphology, and had only trace levels of
DNA ***methyltransferase*** activity. A quantitative end-labeling
assay showed that the level of m5C in the DNA of homozygous mutant cells
was about one-third that of wild-type cells, and Southern blot analysis
after cleavage of the DNA with a methylation-sensitive restriction
endonuclease revealed substantial demethylation of endogenous retroviral
DNA. The mutation was introduced into the germline of mice and found to
cause a recessive lethal phenotype. Homozygous embryos were stunted,
delayed in development, and did not survive past mid-gestation. The DNA of
homozygous embryos showed a reduction of the level of m5C similar to that
of homozygous ES cells. These results indicate that while a 3-fold
reduction in levels of genomic m5C has no detectable effect on the
viability or proliferation of ES cells in culture, a similar reduction of
DNA methylation in embryos causes abnormal development and embryonic
lethality.

L13 ANSWER 7 OF 9 MEDLINE DUPLICATE 3
AN 93046689 MEDLINE
DN 93046689
TI A targeting sequence directs DNA ***methyltransferase*** to sites of
DNA replication in mammalian nuclei.
AU Leonhardt H; Page A W; Weier H U; ***Bestor T H***
CS Department of Anatomy and Cellular Biology, Harvard Medical School,
Boston, Massachusetts 02115.
NC GM43565 (NIGMS)
HD17665 (NICHD)
SO CELL, (1992 Nov 27) 71 (5) 865-73.
Journal code: CQ4. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199302
AB Tissue-specific patterns of methylated deoxycytidine residues in the
mammalian genome are preserved by postreplicative methylation of newly
synthesized DNA. DNA ***methyltransferase*** (MTase) is here shown to
associate with replication foci during S phase but to display a diffuse
nucleoplasmic distribution in non-S phase cells. Analysis of DNA
MTase-beta-galactosidase ***fusion*** proteins has shown that
association with replication foci is mediated by a novel targeting
sequence located near the N-terminus of DNA MTase. This sequence has the
properties expected of a targeting sequence in that it is not required for
enzymatic activity, prevents proper targeting when deleted, and, when
fused to beta-galactosidase, causes the ***fusion*** protein to
associate with replication foci in a cell cycle-dependent manner.

L13 ANSWER 8 OF 9 MEDLINE DUPLICATE 4
AN 92112052 MEDLINE
DN 92112052
TI Expression in mammalian cells of a cloned gene encoding murine DNA
methyltransferase .
AU Czank A; Hauselmann R; Page A W; Leonhardt H; ***Bestor T H*** ;
Schaffner W; Hergersberg M
CS Institut fur Molekularbiologie II, Universitat Zurich, Switzerland.
SO GENE, (1991 Dec 30) 109 (2) 259-63.
Journal code: FOP. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199204
AB Mammalian DNA cytosine-5- ***methyltransferase*** (MTase, EC 2.1.1.37)
is an essential component for establishing and maintaining cell-type
specific methylation patterns in the genome. The cDNA for the murine
enzyme was previously cloned in segments. We have reconstructed the entire
gene, encoding a protein of 1517 amino acids, from a set of overlapping
cDNA clones. We report the assembly of two expression constructs in
bacterial/mammalian shuttle vectors. Transcription in the first construct
(pEMT) is driven by the cytomegalovirus enhancer/promoter and

encodes a
fusion protein with 15 additional aa at the N terminus, while the
second construct (pJMT) is driven by the simian virus 40 early
promoter/enhancer upstream from the natural ATG codon. Immunofluorescence
microscopy and immunoblot analysis have shown that both constructs direct
the synthesis of MTase in COS-1 cells. Enzyme activity in whole-cell
lysates of transfected COS-1 cells transfected with pEMT and pJMT are on
average tenfold and fivefold higher than in controls, respectively. The
specific activities of the recombinant and endogenous mouse-cell enzyme
are similar. These expression constructs will be of use in studies of DNA
methylation in mammals.

L13 ANSWER 9 OF 9 MEDLINE DUPLICATE 5
AN 90175644 MEDLINE
DN 90175644
TI DNA methylation: evolution of a bacterial immune function into a regulator
of gene expression and genome structure in higher eukaryotes.
AU ***Bestor T H***
CS Department of Anatomy and Cellular Biology, Harvard Medical School,
Boston, Massachusetts 02115.
SO PHILOSOPHICAL TRANSACTIONS OF THE ROYAL SOCIETY OF LONDON. SERIES B:
BIOLOGICAL SCIENCES, (1990 Jan 30) 326 (1235) 179-87.
Ref: 32
Journal code: P5Z. ISSN: 0962-8436.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199006
AB The amino acid sequence of mammalian DNA ***methyltransferase*** has
been deduced from the nucleotide sequence of a cloned cDNA. It appears
that the mammalian enzyme arose during evolution via ***fusion*** of a
prokaryotic restriction ***methyltransferase*** gene and a second gene
of unknown function. Mammalian DNA ***methyltransferase*** currently
comprises an N-terminal domain of about 1000 amino acids that may have a
regulatory role and a C-terminal 570 amino acid domain that retains
similarities to bacterial restriction ***methyltransferases*** . The
sequence similarities among mammalian and bacterial DNA cytosine
methyltransferases suggest a common evolutionary origin. DNA
methylation is uncommon among those eukaryotes having genomes of less than
10(8) base pairs, but nearly universal among large-genome eukaryotes. This
and other considerations make it likely that sequence inactivation by DNA
methylation has evolved to compensate for the expansion of the genome that
has accompanied the development of higher plants and animals. As
methylated sequences are usually propagated in the repressed,
nuclease-insensitive state, it is likely that DNA methylation
compartmentalizes the genome to facilitate gene regulation by reducing the
total amount of DNA sequence that must be scanned by DNA-binding
regulatory proteins. DNA methylation is involved in immune recognition in
bacteria but appears to regulate the structure and expression of the
genome in complex higher eukaryotes. I suggest that the DNA-methylating
system of mammals was derived from that of bacteria by way of a
hypothetical intermediate that carried out selective de novo methylation
of exogenous DNA and propagated the methylated DNA in the repressed state
within its own genome.(ABSTRACT TRUNCATED AT 250 WORDS)

=> d his

(FILE 'HOME' ENTERED AT 12:56:27 ON 25 MAR 2001)

FILE 'MEDLINE' ENTERED AT 12:56:33 ON 25 MAR 2001
L1 57 S METHYLTRANSFERASE AND CHIMER?/AB,BI
L2 1 S L1 AND CPG?/AB,BI
L3 0 S L1 AND LEX?/AB,BI
L4 9 S ZINC FINGER AND METHYLTRANSFERASE#/AB,BI
L5 1 S L4 AND (FUSION OR CHIMER?)/AB,BI

FILE 'MEDLINE, EMBASE, BIOSIS, INPADOC, CAPLUS' ENTERED AT 13:00:32 ON 25
MAR 2001
E BESTOR T/AB,BI
E BESTOR T/AU
L6 224 S E3-E8
L7 5 S L1 AND L6
L8 4 DUP REM L7 (1 DUPLICATE REMOVED)
L9 777 S METHYLTRANSFERASE# AND (FUSION OR CHIMER?)/AB,BI
L10 16 S L9 AND CPG/AB,BI
L11 9 DUP REM L10 (7 DUPLICATES REMOVED)
L12 20 S L9 AND L6
L13 9 DUP REM L12 (11 DUPLICATES REMOVED)